

*Search Nts for 10/603108*

<!--StartFragment-->GenCore version 5.1.9

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OM nucleic - nucleic search, using sw model

Run on: December 26, 2006, 16:55:33 ; Search time 751 Seconds  
(without alignments)  
9218.965 Million cell updates/sec

Title: US-10-603-108-1298  
Perfect score: 993  
Sequence: 1 atgctaactttaacagttga.....ccaaaaaaaaatcaagtttag 993

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 8

Total number of hits satisfying chosen parameters: 5740404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : N\_Geneseq\_8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	993	100.0	993	12 ADL03612	Adl03612 DNA encod
2	793	79.9	269223	4 AAF28554	Aaf28554 Genomic f
3	790	79.6	1359	8 ACA38948	Aca38948 Prokaryot
4	648	65.3	1119	12 ADL03329	Adl03329 DNA encod
5	21	2.1	474	10 ACC61620	Acc61620 Gene sequ

	6	21	2.1	474	10	ADK64341	Adk64341 Disease t
	7	20	2.0	60	6	ABN34683	Abn34683 Human spl
	8	20	2.0	425	9	ACH13849	Ach13849 Human adu
	9	20	2.0	496	9	ACH44169	Ach44169 Human foe
	10	20	2.0	557	6	ABQ36870	Abq36870 Oligonucl
c	11	20	2.0	557	6	ABQ36871	Abq36871 Oligonucl
	12	20	2.0	1024	6	ABQ54770	Abq54770 Human ova
	13	20	2.0	1371	4	AAS53339	Aas53339 Haemophil
	14	20	2.0	1371	8	ACA34196	Aca34196 Prokaryot
	15	20	2.0	1371	11	ADL46421	Adl46421 UDP-N-ace
	16	20	2.0	1371	14	AEC10850	Aec10850 Haemophil
	17	20	2.0	1455	3	AAC98882	Aac98882 Human pan
	18	20	2.0	1708	4	AAI60145	Aai60145 Human pol
	19	20	2.0	2007	4	AAI58359	Aai58359 Human pol
	20	20	2.0	2007	5	ADQ98568	Adq98568 DNA encod
	21	20	2.0	2007	9	ADB48328	Adb48328 Novel hum
	22	20	2.0	2850	15	AEE31211	Aee31211 Haemophil
	23	20	2.0	2880	15	AEE31400	Aee31400 Haemophil
	24	20	2.0	25523	13	ADT05538	Adt05538 Haemophil
c	25	20	2.0	106645	13	ADT05645	Adt05645 Haemophil
	26	20	2.0	110000	2	AAT42063_06	Continuation (7 of
c	27	19	1.9	688	4	ABL22443	Abl22443 Drosophil
	28	19	1.9	1434	8	ACA34455	Aca34455 Prokaryot
	29	19	1.9	2379	6	ABS67350	Abs67350 Chlamydia
	30	19	1.9	2379	10	ADD43761	Add43761 Chlamydia
	31	19	1.9	2379	14	AEA19053	Aea19053 Chlamydia
	32	19	1.9	3485	4	ABL22442	Abl22442 Drosophil
c	33	19	1.9	3780	13	ADS89656	Ads89656 Oligonucl
	34	19	1.9	4333	4	ABL07040	Abl07040 Drosophil
	35	19	1.9	8200	4	ABL07024	Abl07024 Drosophil
	36	19	1.9	9302	13	ADT05516	Adt05516 Haemophil
c	37	19	1.9	9524	6	ABK39993	Abk39993 Human che
c	38	19	1.9	9524	6	ABL32838	Abl32838 Human imm
	39	19	1.9	15147	13	ADT05641	Adt05641 Haemophil
c	40	19	1.9	15853	6	ABL70466	Abl70466 Chemicall
c	41	19	1.9	15853	6	AAS61457	Aas61457 Human gen
c	42	19	1.9	80321	11	ACN45012	Acn45012 Mouse gen
c	43	19	1.9	110000	2	AAT42063_08	Continuation (9 of
	44	19	1.9	110000	2	AAT42063_14	Continuation (15 o
c	45	19	1.9	110000	5	AAI61373_3	Continuation (4 of

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<!--StartFragment-->GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2006, 17:09:12 ; Search time 5793 Seconds  
 (without alignments)  
 10961.469 Million cell updates/sec

Title: US-10-603-108-1298  
 Perfect score: 993  
 Sequence: 1 atgctaactttaacagttga.....ccaaaaaaatcaagtttag 993

Scoring table: OLIGO\_NUC  
 Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 8

Total number of hits satisfying chosen parameters: 10367082

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : GenEmbl:\*  
 1: gb\_env:\*  
 2: gb\_pat:\*  
 3: gb\_ph:\*  
 4: gb\_pl:\*  
 5: gb\_pr:\*  
 6: gb\_ro:\*  
 7: gb\_sts:\*  
 8: gb\_sy:\*  
 9: gb\_un:\*  
 10: gb\_vi:\*  
 11: gb\_ov:\*  
 12: gb\_htg:\*  
 13: gb\_in:\*  
 14: gb\_om:\*  
 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	993	100.0	993	2	AR450634	AR450634 Sequence
2	793	79.9	269223	2	AR408762	AR408762 Sequence
3	793	79.9	269223	2	AX067466	AX067466 Sequence
4	648	65.3	1119	2	AR450351	AR450351 Sequence
5	23	2.3	165217	12	CT027727	CT027727 Danio rer

	6	23	2.3	214513	11	BX950853	BX950853 Zebrafish
c	7	22	2.2	164550	5	CNS01RHY	AL162633 Human chr
	8	22	2.2	175988	5	CNS05TC7	AL355073 Human chr
c	9	22	2.2	198278	12	AC010097	AC010097 Homo sapi
	10	22	2.2	213316	12	AC160948	AC160948 Bos tauru
c	11	22	2.2	233753	12	AC137805	AC137805 Homo sapi
	12	21	2.1	474	2	AX596368	AX596368 Sequence
	13	21	2.1	474	2	AX820660	AX820660 Sequence
	14	21	2.1	474	2	AX831690	AX831690 Sequence
c	15	21	2.1	868	4	SCYGR076C	Z72861 S.cerevisia
	16	21	2.1	1449	4	SCYMR26	X56106 S.cerevisia
c	17	21	2.1	110000	4	AP008216_190	Continuation (191
c	18	21	2.1	110000	4	AE016959_190	Continuation (191
	19	21	2.1	110000	4	AP007159_09	Continuation (10 o
	20	21	2.1	115023	4	AC138527	AC138527 Medicago
	21	21	2.1	119370	12	AC105930	AC105930 Magnaport
	22	21	2.1	151991	4	AC091122	AC091122 Oryza sat
	23	21	2.1	167152	6	AC163393	AC163393 Mus muscu
c	24	21	2.1	168536	12	AC162268	AC162268 Bos tauru
c	25	21	2.1	173239	5	AC016399	AC016399 Homo sapi
	26	21	2.1	176188	5	AC068898	AC068898 Homo sapi
c	27	21	2.1	186014	11	BX908749	BX908749 Zebrafish
	28	21	2.1	192706	12	AC173393	AC173393 Bos tauru
c	29	21	2.1	208154	11	CR788244	CR788244 Zebrafish
	30	21	2.1	215498	11	BX547927	BX547927 Zebrafish
	31	21	2.1	223952	6	AC107742	AC107742 Mus muscu
c	32	21	2.1	254436	13	AE014827	AE014827 Plasmodiu
	33	20	2.0	60	2	CQ537796	CQ537796 Sequence
	34	20	2.0	687	13	CT033675	CT033675 Platynere
c	35	20	2.0	687	13	CT033676	CT033676 Platynere
	36	20	2.0	699	13	CT032677	CT032677 Platynere
	37	20	2.0	704	13	CT032567	CT032567 Platynere
c	38	20	2.0	704	13	CT032568	CT032568 Platynere
c	39	20	2.0	720	13	CT032678	CT032678 Platynere
c	40	20	2.0	1221	13	AY039360	AY039360 Onthophag
	41	20	2.0	1368	2	CS222758	CS222758 Sequence
	42	20	2.0	1371	2	AX932186	AX932186 Sequence
	43	20	2.0	2007	2	AR338747	AR338747 Sequence
	44	20	2.0	2109	5	AK026760	AK026760 Homo sapi
	45	20	2.0	2222	5	AK124047	AK124047 Homo sapi

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<!--StartFragment-->GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2006, 17:44:59 ; Search time 5675 Seconds  
 (without alignments)  
 9784.651 Million cell updates/sec

Title: US-10-603-108-1298  
 Perfect score: 993  
 Sequence: 1 atgctaactttaacagttga.....ccaaaaaaatcaagtttag 993

Scoring table: OLIGO\_NUC  
 Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 8

Total number of hits satisfying chosen parameters: 94430840

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est3:\*  
 3: gb\_est4:\*  
 4: gb\_est5:\*  
 5: gb\_est6:\*  
 6: gb\_htc:\*  
 7: gb\_est2:\*  
 8: gb\_est7:\*  
 9: gb\_est8:\*  
 10: gb\_est9:\*  
 11: gb\_gss1:\*  
 12: gb\_gss2:\*  
 13: gb\_gss3:\*  
 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
c	1	23	2.3	289	14	CT011940	CT011940 KBrH119N1
c	2	23	2.3	367	14	CT012055	CT012055 KBrH119N1
c	3	23	2.3	907	13	DU114572	DU114572 KBrH096K1
c	4	22	2.2	671	9	DN537400	DN537400 1373575 M
	5	22	2.2	717	9	DN535975	DN535975 1372039 M
	6	22	2.2	721	10	DT891184	DT891184 1472302 M

c	7	22	2.2	729	10	DT889825	DT889825 1470766 M
	8	22	2.2	797	10	DV183743	DV183743 CT026_F03
c	9	21	2.1	379	14	T09797	T09797 0378m7 gmbP
c	10	21	2.1	426	13	CW448297	CW448297 fsbb001f1
c	11	21	2.1	669	13	CW059644	CW059644 104_302_1
c	12	21	2.1	686	8	CV718881	CV718881 UCRCS08_0
	13	21	2.1	690	8	CV718880	CV718880 UCRCS08_0
c	14	21	2.1	694	13	CW435175	CW435175 fsbb001f1
c	15	21	2.1	744	10	DW581574	DW581574 EST_ssal_
c	16	21	2.1	757	13	DU127507	DU127507 KBrH108M2
	17	21	2.1	761	8	CX075188	CX075188 UCRCS08_4
	18	21	2.1	770	11	AZ210845	AZ210845 SP_0153_B
c	19	21	2.1	775	8	CX047009	CX047009 UCRCS09_1
	20	21	2.1	806	8	CX047008	CX047008 UCRCS09_1
c	21	21	2.1	812	8	CX053775	CX053775 UCRCS09_8
	22	21	2.1	816	8	CX053774	CX053774 UCRCS09_8
c	23	21	2.1	877	12	CG956559	CG956559 MBEKJ23TR
	24	21	2.1	1210	14	AG323994	AG323994 Mus muscu
	25	20	2.0	277	8	CN824930	CN824930 96 Nicoti
	26	20	2.0	350	7	BE170924	BE170924 QV3-HT054
c	27	20	2.0	360	1	AM142296	AM142296 AM142296
	28	20	2.0	362	1	AV659387	AV659387 AV659387
c	29	20	2.0	369	2	BF756568	BF756568 QV3-CT055
	30	20	2.0	376	10	DR900809	DR900809 JGI_XZT54
c	31	20	2.0	377	8	CO987375	CO987375 UMC-pd10e
	32	20	2.0	399	4	BY396352	BY396352 BY396352
c	33	20	2.0	418	1	AV670216	AV670216 AV670216
	34	20	2.0	424	7	AW802965	AW802965 IL2-UM007
c	35	20	2.0	427	1	AM155260	AM155260 AM155260
c	36	20	2.0	433	1	AU179366	AU179366 AU179366
	37	20	2.0	444	1	AI393324	AI393324 tg44a08.x
c	38	20	2.0	449	14	AL754153	AL754153 Arabidops
	39	20	2.0	462	4	BW571097	BW571097 BW571097
c	40	20	2.0	487	4	BX112993	BX112993 BX112993
c	41	20	2.0	489	8	CX103703	CX103703 BI027C21
	42	20	2.0	490	12	CG065161	CG065161 PUIBY17TB
	43	20	2.0	537	9	DA841670	DA841670 DA841670
	44	20	2.0	540	13	CW105344	CW105344 104_474_1
c	45	20	2.0	550	1	AV669211	AV669211 AV669211

&lt;!--EndFragment--&gt;

<!--StartFragment-->GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: December 26, 2006, 15:16:56 ; Search time 203 Seconds  
 (without alignments)  
 743.258 Million cell updates/sec

Title: US-10-603-108-3218  
 Perfect score: 1692  
 Sequence: 1 MLTLTVDKPFGLGRIVRNQG.....LARAKQATIIGWSRPKKNQV 330

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1692	100.0	330	8	ADL05532	Adl05532 M. catarr
2	1669	98.6	453	6	ABU35078	Abu35078 Protein e
3	1242	73.4	372	8	ADL05249	Adl05249 M. catarr
4	965	57.0	454	6	ABU16817	Abu16817 Protein e
5	965	57.0	461	6	ADA33820	Ada33820 Acinetoba
6	891	52.7	458	6	ABU39487	Abu39487 Protein e
7	877	51.8	456	4	AAU35480	Aau35480 Haemophil
8	877	51.8	456	6	ABU30326	Abu30326 Protein e
9	877	51.8	456	7	ADL46422	Adl46422 UDP-N-ace
10	877	51.8	456	9	AEC10851	Aec10851 Haemophil

11	877	51.8	456	10	AEE31345	Aee31345 Haemophil
12	875	51.7	453	6	ABU49642	Abu49642 Protein e
13	873	51.6	456	7	ADL46424	Adl46424 UDP-N-ace
14	873	51.6	456	9	AEC10853	Aec10853 Haemophil
15	862	50.9	456	6	ABU50612	Abu50612 Protein e
16	855.5	50.6	457	6	ABU41088	Abu41088 Protein e
17	855.5	50.6	493	7	ADF07235	Adf07235 Bacterial
18	854	50.5	380	8	ADI38913	Adi38913 N-termina
19	854	50.5	456	4	AAU34807	Aau34807 E. coli c
20	854	50.5	456	6	ABU28830	Abu28830 Protein e
21	854	50.5	456	8	ADI38911	Adi38911 glmU, SEQ
22	839	49.6	458	6	ABM70564	Abm70564 Photorhab
23	837	49.5	456	6	ABU28357	Abu28357 Protein e
24	832	49.2	456	6	ABU48227	Abu48227 Protein e
25	827	48.9	456	4	AAU38471	Aau38471 Salmonell
26	827	48.9	458	4	AAU36166	Aau36166 Klebsiell
27	827	48.9	458	6	ABU31195	Abu31195 Protein e
28	827	48.9	474	7	ABO64180	Abo64180 Klebsiell
29	815.5	48.2	461	9	AEB42140	Aeb42140 L. pneumo
30	812.5	48.0	425	6	ABU33617	Abu33617 Protein e
31	809.5	47.8	456	8	ADP08171	Adp08171 Neisseria
32	802.5	47.4	471	6	ABU37628	Abu37628 Protein e
33	797.5	47.1	456	6	ABU37751	Abu37751 Protein e
34	791.5	46.8	471	6	ABP77136	Abp77136 N. gonorr
35	791.5	46.8	471	6	ABU37558	Abu37558 Protein e
36	779.5	46.1	453	6	ABU19390	Abu19390 Protein e
37	778.5	46.0	406	6	ABU40340	Abu40340 Protein e
38	769.5	45.5	455	6	ABU41713	Abu41713 Protein e
39	766.5	45.3	566	6	ABU22204	Abu22204 Protein e
40	762.5	45.1	457	6	ABU23281	Abu23281 Protein e
41	759.5	44.9	453	6	ABU21474	Abu21474 Protein e
42	752.5	44.5	454	4	AAU36519	Aau36519 Pseudomon
43	752.5	44.5	454	6	ABU38925	Abu38925 Protein e
44	752.5	44.5	462	7	ABO70256	Abo70256 Pseudomon
45	697	41.2	409	6	ABU31446	Abu31446 Protein e

<!--EndFragment-->



<!--StartFragment-->GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: December 26, 2006, 15:17:35 ; Search time 303 Seconds  
 (without alignments)  
 1007.443 Million cell updates/sec

Title: US-10-603-108-3218  
 Perfect score: 1692  
 Sequence: 1 MLTLTVDKPFGLGRIVRNQG.....LARAKQATIIGWSRPKKNQV 330

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt\_7.2:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1069.5	63.2	458	2	Q4FPY8_PSYAR	Q4fpy8 psychrobact
2	1054.5	62.3	458	2	Q3GS42_9GAMM	Q3gs42 psychrobact
3	939	55.5	454	2	Q6F6U9_ACIAD	Q6f6u9 acinetobact
4	927.5	54.8	452	2	Q2S6P3_9GAMM	Q2s6p3 hahella che
5	909.5	53.8	454	2	Q36LW9_MARHY	Q36lw9 marinobacte
6	893	52.8	462	2	Q2YCA1_NITMU	Q2ycal nitrosospir
7	891	52.7	458	2	Q9CK29_PASMU	Q9ck29 pasteurella
8	889	52.5	454	2	Q2X1G8_9GAMM	Q2x1g8 shewanella
9	889	52.5	454	2	Q2ZQL4_SHEPU	Q2zql4 shewanella
10	887	52.4	457	2	Q65R54_MANSM	Q65r54 mannheimia
11	886	52.4	452	2	Q3IK30_PSEHT	Q3ik30 pseudoalter
12	885	52.3	454	2	Q8E8C2_SHEON	Q8e8c2 shewanella
13	884	52.2	460	2	Q3Q816_9GAMM	Q3q816 shewanella
14	884	52.2	461	2	Q47UE0_COLP3	Q47ue0 colwellia p
15	883	52.2	454	2	Q35V62_9GAMM	Q35v62 shewanella
16	883	52.2	454	2	Q366Q8_9GAMM	Q366q8 shewanella
17	880	52.0	454	2	Q2Z4D6_9GAMM	Q2z4d6 shewanella
18	880	52.0	456	2	Q4QMS5_HAEI8	Q4qms5 haemophilus

19	879	52.0	454	2	Q3NKZ0_SHEFR	Q3nkz0 shewanella
20	878.5	51.9	454	2	Q31DM2_THICR	Q31dm2 thiomicrosp
21	877	51.8	456	1	GLMU_HAEIN	P43889 haemophilus
22	875	51.7	453	2	Q9KNH7_VIBCH	Q9knh7 vibrio chol
23	865.5	51.2	456	2	Q44KV5_CHRSL	Q44kv5 chromohalob
24	862	50.9	456	2	Q663R0_YERPS	Q663r0 yersinia ps
25	862	50.9	456	2	Q8Z9S7_YERPE	Q8z9s7 yersinia pe
26	862	50.9	458	2	Q8CZF5_YERPE	Q8czf5 yersinia pe
27	860	50.8	452	2	Q5E1N9_VIBF1	Q5e1n9 vibrio fisc
28	860	50.8	454	2	Q3EFK4_ACTSC	Q3efk4 actinobacil
29	858	50.7	456	2	Q3YVN4_SHISS	Q3yvn4 shigella so
30	858	50.7	458	2	Q3SF69_THIDA	Q3sf69 thiobacillu
31	857	50.7	453	2	Q7MGI2_VIBVY	Q7mgi2 vibrio vuln
32	857	50.7	456	2	Q8FBT3_ECOL6	Q8fbt3 escherichia
33	854	50.5	456	1	GLMU_ECO57	P0acc8 escherichia
34	854	50.5	456	1	GLMU_ECOLI	P0acc7 escherichia
35	854	50.5	456	2	Q329R9_SHIDS	Q329r9 shigella dy
36	854	50.5	456	2	Q2M848_ECOLI	Q2m848 escherichia
37	853	50.4	453	2	Q8DDG6_VIBVU	Q8ddg6 vibrio vuln
38	852.5	50.4	452	2	Q47JK2_DECAR	Q47jk2 dechloromon
39	852	50.4	454	2	Q3P1W4_9GAMM	Q3p1w4 shewanella
40	851	50.3	456	2	Q83IY3_SHIFL	Q83iy3 shigella fl
41	850	50.2	453	2	Q87KB0_VIBPA	Q87kb0 vibrio para
42	849.5	50.2	456	2	Q5QZH4_IDILO	Q5qzh4 idiomarina
43	849	50.2	454	2	Q33SJ0_9GAMM	Q33sj0 shewanella
44	849	50.2	456	2	Q31UN0_SHIBS	Q31un0 shigella bo
45	847	50.1	456	2	Q6CYJ8_ERWCT	Q6cyj8 erwinia car

<!--EndFragment-->